

# Raw Sequence Listing Error Summary

#16

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: \_\_\_\_\_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
      Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2        Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3        Misaligned Amino  
      Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4        Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5        Variable Length      Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6        PatentIn 2.0  
      "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7        Skipped Sequences  
      (OLD RULES)      Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
      (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
      This sequence is intentionally skipped  
  
      Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8        Skipped Sequences  
      (NEW RULES)      Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
      <210> sequence id number  
      <400> sequence id number  
      000
- 9        Use of n's or Xaa's  
      (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
      In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10        Invalid <213>  
      Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11        Use of <220>      Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12        PatentIn 2.0  
      "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13        Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

*Invalid response for field 211.  
Improper format for amino acid sequences; should be 16 per line*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Grn

edit authorized by examiner

CRF Errors Corrected by the STIC System Branch

Serial Number: 09/231,4220

CRF Processing Date: 7/24/2001  
Edited by: \_\_\_\_\_  
Verified by: \_\_\_\_\_ (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☒ Deleted extra, invalid, headings used by an applicant, specifically:  
integer length globally
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

OIPE

## RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/231,422D

TIME: 14:58:58

Input Set : A:\'422 Sequence Listing ASCII 07-01.txt

Output Set: N:\CRF3\07242001\I231422D.raw

4 &lt;110&gt; APPLICANT: Cantor, Thomas L.

6 &lt;120&gt; TITLE OF INVENTION: Methods, Kits, and Antibodies for Detecting Parathyroid

Hormone

W--&gt; 0 &lt;130&gt; FILE REFERENCE:

8 &lt;140&gt; CURRENT APPLICATION NUMBER: US 09/231,422D

10 &lt;141&gt; CURRENT FILING DATE: 1999-01-14

12 &lt;160&gt; NUMBER OF SEQ ID NOS: 6

14 &lt;170&gt; SOFTWARE: Microsoft Word 2000 - ASCII format

17 &lt;210&gt; SEQ ID NO: 1

19 &lt;211&gt; LENGTH: 7 [integer length]

21 &lt;212&gt; TYPE: PRT

23 &lt;213&gt; ORGANISM: human parathyroid hormone peptide fragment

25 &lt;400&gt; SEQUENCE: 1

27 Ser Val Ser Glu Ile Gln Leu

28 1 5

31 &lt;210&gt; SEQ ID NO: 2

33 &lt;211&gt; LENGTH: 84 [integer length]

35 &lt;212&gt; TYPE: PRT

37 &lt;213&gt; ORGANISM: human parathyroid hormone peptide fragment

39 &lt;400&gt; SEQUENCE: 2

41 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu

42 1 5 10 15

44 Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp

45 20 25 30

47 Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp

48 35 40 45

50 Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val

51 50 55 60

53 Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asp Lys Ala Asp Val

54 65 70 75

56 Asn Val Leu Thr Lys Ala Lys Ser Gln

57 80

60 &lt;210&gt; SEQ ID NO: 3

62 &lt;211&gt; LENGTH: 7 [integer length]

64 &lt;212&gt; TYPE: PRT

66 &lt;213&gt; ORGANISM: human parathyroid hormone peptide fragment

68 &lt;400&gt; SEQUENCE: 3

70 Val Ser Glu Ile Gln Leu Met

71 1 5

74 &lt;210&gt; SEQ ID NO: 4

76 &lt;211&gt; LENGTH: 8 [integer length]

78 &lt;212&gt; TYPE: PRT

80 &lt;213&gt; ORGANISM: human parathyroid hormone peptide fragment

82 &lt;400&gt; SEQUENCE: 4

84 Ser Val Ser Glu Ile Gln Leu Met

85 1 5

88 &lt;210&gt; SEQ ID NO: 5

90 &lt;211&gt; LENGTH: 8 [integer length]

Does Not Comply  
Corrected Diskette NeededThe only acceptable response in the  
211 field should be the appropriate  
integer. No erroneous  
additional messages or alpha  
characters are acceptable for this  
field. MTFormat incorrect  
should be 16 amino  
acids per line

## RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/231,422D

TIME: 14:58:58

Input Set : A:\'422 Sequence Listing ASCII 07-01.txt

Output Set: N:\CRF3\07242001\I231422D.raw

92 &lt;212&gt; TYPE: PRT

94 &lt;213&gt; ORGANISM: rat parathyroid hormone peptide fragment

96 &lt;400&gt; SEQUENCE: 5

98 Ala Val Ser Glu Ile Gln Leu Met

99 1 5

102 &lt;210&gt; SEQ ID NO: 6

104 &lt;211&gt; LENGTH: 78 [integer length]

106 &lt;212&gt; TYPE: PRT

108 &lt;213&gt; ORGANISM: human parathyroid hormone peptide fragment

110 &lt;400&gt; SEQUENCE: 6

112 Leu Met His Asn Leu Gly Lys His Leu Asn Ser Met Glu Arg Val

113 1 5 10 15

115 Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His Asn Phe Val Ala

116 20 25 30

118 Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser Gln Arg Pro

119 35 40 45

121 Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His Glu Lys Ser

122 50 55 60

124 Leu Gly Glu Ala Asp Lys Ala Asp Val Asn Val Leu Thr Lys Ala

125 65 70 75

127 Lys Ser Gln

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/231,422D

DATE: 07/24/2001

TIME: 14:58:59

Input Set : A:\'422 Sequence Listing ASCII 07-01.txt

Output Set: N:\CRF3\07242001\I231422D.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE